

SEQUENCE LISTING

<110> Bender, Eckhard  
 Pindon, Armelle N  
 Van Oers, Irma P  
 Jurzak, Mirek  
 Luyten, Walter H

<120> Cloning and expression of a novel 5-HT4 receptor

<130> Novel 5HT4B splice variant

<140> PCT/EP00/05592

<141> 2000-06-14

<150> GB/9913850.5

<151> 1999-06-14

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (4)..(1209)

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tca gtg gag aag gtg gtg ctg ctc acg ttt ctc tcg acg gtt atc ctg	96
Ser Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu	
20 25 30	

atg gcc atc ttg ggg aac ctg ctg gtg atg gtg gct gtg tgc tgg gac	144
Met Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp	
35 40 45	

agg cag ctc agg aaa ata aaa aca aat tat ttc att gta tct ctt gct	192
Arg Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala	
50 55 60	

ttt gcg gat ctg ctg gtt tcg gtg ctg gtg atg ccc ttt ggt gcc att	240
Phe Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile	
65 70 75	

gag ctg gtt caa gac atc tgg att tat ggg gag gtg ttt tgt ctt gtt	288
Glu Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val	
80 85 90 95	

cgg aca tct ctg gac gtc ctg ctc aca acg gca tcg att ttt cac ctg	336
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Arg	Thr	Ser	Leu	Asp	Val	Leu	Leu	Thr	Thr	Ala	Ser	Ile	Phe	His	Leu	
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tgc	tgc	att	tct	ctg	gat	agg	tat	tac	gcc	atc	tgc	tgc	cag	cct	ttg	384
Cys	Cys	Ile	Ser	Leu	Asp	Arg	Tyr	Tyr	Ala	Ile	Cys	Cys	Gln	Pro	Leu	
			115					120					125			
gtc	tat	agg	aac	aag	atg	acc	cct	ctg	cgc	atc	gca	tta	atg	ctg	gga	432
Val	Tyr	Arg	Asn	Lys	Met	Thr	Pro	Leu	Arg	Ile	Ala	Leu	Met	Leu	Gly	
		130					135					140				
ggc	tgc	tgg	gtc	atc	ccc	acg	ttt	att	tct	ttt	ctc	cct	ata	atg	caa	480
Gly	Cys	Trp	Val	Ile	Pro	Thr	Phe	Ile	Ser	Phe	Leu	Pro	Ile	Met	Gln	
	145					150				155						
ggc	tgg	aat	aac	att	ggc	ata	att	gat	ttg	gaa	agg	agt	cta	aac	caa	528
Gly	Trp	Asn	Asn	Ile	Gly	Ile	Ile	Asp	Leu	Glu	Arg	Ser	Leu	Asn	Gln	
	160				165				170						175	
ggc	ctg	ggc	cag	gat	ttt	cat	gcg	ata	gaa	aag	agg	aag	ttc	aac	cag	576
Gly	Leu	Gly	Gln	Asp	Phe	His	Ala	Ile	Glu	Lys	Arg	Lys	Phe	Asn	Gln	
			180						185					190		
aac	tct	aac	tct	acg	tac	tgt	gtc	ttc	atg	gtc	aac	aag	ccc	tac	gcc	624
Asn	Ser	Asn	Ser	Thr	Tyr	Cys	Val	Phe	Met	Val	Asn	Lys	Pro	Tyr	Ala	
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atc	acc	tgc	tct	gtg	gtg	gcc	ttc	tac	atc	cca	ttt	ctc	ctc	atg	gtg	672
Ile	Thr	Cys	Ser	Val	Val	Ala	Phe	Tyr	Ile	Pro	Phe	Leu	Leu	Met	Val	
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ctg	gcc	tat	tac	cgc	atc	tat	gtc	aca	gct	aag	gag	cat	gcc	cat	cag	720
Leu	Ala	Tyr	Tyr	Arg	Ile	Tyr	Val	Thr	Ala	Lys	Glu	His	Ala	His	Gln	
	225					230					235					
atc	cag	atg	tta	caa	cgg	gca	gga	gcc	tcc	tcc	gag	agc	agg	cct	cag	768
Ile	Gln	Met	Leu	Gln	Arg	Ala	Gly	Ala	Ser	Ser	Glu	Ser	Arg	Pro	Gln	
	240				245				250					255		
tcg	gca	gac	cag	cat	agc	act	cat	cgc	atg	agg	aca	gag	acc	aaa	gca	816
Ser	Ala	Asp	Gln	His	Ser	Thr	His	Arg	Met	Arg	Thr	Glu	Thr	Lys	Ala	
			260					265						270		
gcc	aag	acc	ctg	tgc	atc	atc	atg	ggt	tgc	ttc	tgc	ctc	tgc	tgg	gca	864
Ala	Lys	Thr	Leu	Cys	Ile	Ile	Met	Gly	Cys	Phe	Cys	Leu	Cys	Trp	Ala	
			275					280					285			
cca	ttc	ttt	gtc	acc	aat	att	gtg	gat	cct	ttc	ata	gac	tac	act	gtc	912
Pro	Phe	Phe	Val	Thr	Asn	Ile	Val	Asp	Pro	Phe	Ile	Asp	Tyr	Thr	Val	
		290					295					300				
cct	ggg	cag	gtg	tgg	act	gct	ttc	ctc	tgg	ctc	ggc	tat	atc	aat	tcc	960
Pro	Gly	Gln	Val	Trp	Thr	Ala	Phe	Leu	Trp	Leu	Gly	Tyr	Ile	Asn	Ser	
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ggg	ttg	aac	cct	ttt	ctc	tac	gcc	ttc	ttg	aat	aag	tct	ttt	aga	cgt	1008
Gly	Leu	Asn	Pro	Phe	Leu	Tyr	Ala	Phe	Leu	Asn	Lys	Ser	Phe	Arg	Arg	

320	325	330	335	
gcc ttc ctc atc atc ctc tgc tgt gat gat gag cgc tac cga aga cct				1056
Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro				
340		345	350	
tcc att ctg ggc cag act gtc cct tgt tca acc aca acc att aat gga				1104
Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly				
355		360	365	
tcc aca cat gta cta agg gat gca gtg gag tgt ggt ggc cag tgg gag				1152
Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp Glu				
370		375	380	
agt cag tgt cac ccg cca gca act tct cct ttg gtg gct gct cag ccc				1200
Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln Pro				
385		390	395	
agt gac act taggccccctg ggacaatgac ccagaagaca gccatgcctc				1249
Ser Asp Thr				
400				
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Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg			
35	40	45	
Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe			
50	55	60	
Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu			
65	70	75	80
Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg			
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Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys			
100	105	110	
Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val			
115	120	125	
Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly			
130	135	140	

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly  
 145 150 155 160  
 Trp Asn Asn Ile Gly Ile Ile Asp Leu Glu Arg Ser Leu Asn Gln Gly  
 165 170 175  
 Leu Gly Gln Asp Phe His Ala Ile Glu Lys Arg Lys Phe Asn Gln Asn  
 180 185 190  
 Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr Ala Ile  
 195 200 205  
 Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met Val Leu  
 210 215 220  
 Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His Gln Ile  
 225 230 235 240  
 Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro Gln Ser  
 245 250 255  
 Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys Ala Ala  
 260 265 270  
 Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp Ala Pro  
 275 280 285  
 Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr Val Pro  
 290 295 300  
 Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn Ser Gly  
 305 310 315 320  
 Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg Arg Ala  
 325 330 335  
 Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro Ser  
 340 345 350  
 Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly Ser  
 355 360 365  
 Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp Glu Ser  
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 Asp Thr

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cttcatgggtc aacaagccct ac                                     22

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<222> (23)..(24)
<223> V = a or g or c; Y = t or c

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<210> 5
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cgcatgaaaa tcttgccca ggccttggtt                               30

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caagcagcag cttaggacct g 21

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<220>  
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<400> 9  
graayaagat gaccctctr cgyatc 26

<210> 10  
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<222> (5)..(6)  
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26

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<220>  
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<223> s = g or c

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<220>  
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31

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29

<210> 13  
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<220>  
<223> Description of Artificial Sequence: DNA primer

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30